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OM protein - protein search, using sw model

Run on: November 30, 2002, 12:26:53 : Search time 21.3238 Seconds  
(Without alignments)  
2795.154 Million cell updates/sec

Title: US-10-054-680-4

Perfect score: 3228  
Sequence: 1 MAMLRQLPPLTSATLHFGVLTV.....ADYGRGCGEDSRDGRASIG 620

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR\_73:\*  
2: PIR1:\*  
3: PIR2:\*  
4: PIR3:\*  
5: PIR4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2159.5	66.9	970	2 A36417	Na+/Ca2+-exchanging
2	2147.5	66.5	970	2 S27114	Na+/Ca2+-exchanging
3	2146.5	66.5	973	2 S32815	Na+/Ca2+-exchanging
4	2142.5	66.4	970	2 I48097	Na+/Ca2+-exchanging
5	2138	66.2	957	2 A53789	Na+/Ca2+-exchanging
6	2136.5	66.2	941	2 B53335	Na+/Ca2+-exchanging
7	2135.5	66.2	935	2 S43730	Na+/Ca2+-exchanging
8	2135.5	66.2	938	2 S32435	Na+/Ca2+-exchanging
9	2129.5	66.0	971	2 S28833	Na+/Ca2+-exchanging
10	1954.5	60.5	921	2 A54139	Na+/Ca2+-exchanging
11	1196.5	37.1	890	2 B89047	protein C1068.5 [1
12	633.5	19.6	807	2 T24110	hypothetical prote
13	362.5	11.2	538	2 T00424	probable Na+/Ca2+
14	205	6.4	1014	2 T31433	Na+/Ca2+,K+-exchan
15	198.5	6.1	1199	2 S20969	Na+/Ca2+,K+-exchan
16	187	5.8	4936	2 AH2515	hypothetical prote
17	178.5	5.5	591	2 T19746	hypothetical prote
18	170	5.3	611	2 T21747	hypothetical prote
19	169.5	5.3	3016	2 S77300	hypothetical prote
20	166	5.1	1568	2 T08616	aggregation factor
21	156.5	4.8	2205	2 T08615	aggregation factor
22	150.5	4.7	591	2 S40705	Na+/Ca2+,K+-exchan
23	144.5	4.5	703	2 T03888	Na+/Ca2+,K+-exchan
24	144	4.5	644	2 B96582	hypothetical prote
25	144	4.5	1428	2 AC2234	hypothetical prote
26	132	4.1	1807	2 JC6319	integrin beta-4 ch
27	131.5	4.1	826	2 AB1841	hypothetical prote
28	131	4.1	590	2 S40707	hypothetical prote
29	126.5	3.9	1875	2 A36429	integrin beta-4 ch

30	126	3.9	4199	2 S76412	hypothetical prote
31	124	3.8	318	2 A83708	hypothetical prote
32	122	3.8	825	2 T08617	aggregation factor
33	121.5	3.8	651	2 T03889	Na+/Ca2+,K+-exchan
34	121.5	3.8	743	2 T38674	probable membrane
35	119.5	3.7	433	2 S74922	hypothetical prote
36	119	3.7	3972	2 S75251	hypothetical prote
37	115	3.6	324	2 A10434	probable sodium/ca
38	114	3.5	1748	2 JN0786	integrin beta-4 ch
39	113	3.5	332	2 H82064	conserved hypothet
40	112.5	3.5	375	2 I40554	rap60 protein - Ba
41	110	3.4	2397	1 A55535	versican precursor
42	109	3.4	769	2 G95270	hypothetical prote
43	108.5	3.4	652	2 A37000	leukemia virus rec
44	108	3.3	673	1 VCPV85	coat protein vp1 -
45	107.5	3.3	1263	2 T00649	hypothetical prote

## ALIGNMENTS

RESULT 1	
A36417	Na+/Ca2+-exchanging protein - dog
C:Species:	Canis lupus familiaris (dog)
C:Date:	12-Apr-1991 #sequence_revision 12-Apr-1991 #text_change 18-Aug-2000
C:Accession:	A36417
R:Nicolli, D.A.; Longoni, S.; Philipson, K.D.	Science 250, 562-565, 1990
A:Title:	Molecular cloning and functional expression of the cardiac sarcolemmal Na(+)
A:Reference number:	A36417; MIMD:91047958; PMID:1700476
A:Accession:	A36417
A>Status:	preliminary
A:Molecule type:	mRNA
A:Residues:	1-970 <NIC>
A:Cross-references:	GB:M57523; NID:g164072; PION:AAA62766.1; PID:g164073; GB:M36119
C:Superfamily:	human Na+/Ca2+-exchanging protein
C:Keywords:	phosphoprotein; transmembrane protein
Query Match	66.9%; Score 2159.5; DB 2; Length 970;
Best Local Similarity	69.9%; Pred. No. 2.9e-157;
Matches	425; Conservative 73; Mismatches 89; Indels 21; Gaps 8;
QY	1 MAMLRQLPPLTSATLHFGVLTVLR--LNGLRABAGSGDVPSTQNNESGSSDCKEGV 58
DB	1 MLOQLRLPFTSMGCHLAVVALLFSDHLDLSAETEMEGNETGE---CTGSYCKKGV 56
QY	59 ILPIWYEPNPSLGGKIRAVIVYFVALIYMFGLVSTIADRFMASTLEVITSOBREVTIKKPN 118
DB	57 ILPIWEPDPSFGDKIRAVIYFVAAMYMFGLVSTIADRFMSSLEVITSOBREVTIKKPN 116
QY	119 GETSTTIRVNNETVSNLTALGSSAPEILLSTLEVCGHGFIGDLGPSTIVGSAFNM 178
DB	117 GETTKTVIRINNENVTNLTALGSSAPEILLSTLEVCGHGFITAGDLGPSTIVGSAFNM 176
QY	179 FIITGICVYVLPDETRIKRLRVFTTAANSFATYITLVIITLAVSPGCVQVREGILTL 238
DB	177 FIITALCVYVLPDETRIKRLRVFTTAANSFATYITLVIITLAVSPGCVVEVEGLTTF 236
QY	239 FFFPVCVLLAVNADKRLLFYKMHKKVTRDKHGIIEETEDDHKGG---IPMDKMMNSH 295
DB	237 FFFPICVVFANVADKRLLFYKTRIRAGKRGKRIIEHEDRPSKTEIMDKVNVNSH 296
QY	296 ---FLDGNVPLLEGEVD---ESRREMRILKDKOKHPEKDDQLVEMANYALSHQ 348
DB	297 VDNFLDGLVLR--LEVDERDQDEDEARERARILKELKQHPKEIKQLIELANVQLSQQ 355
QY	349 KSRAFYRIQATRMATGAGNITLKKAAEDAKKASSMSEVNHDEPE-DPTSKYFPDPCSYQC 407
DB	356 KSRAFYRIQATRLMTGAGNITLKKRAADAKRAVSMHEVNEVAVENDPVSKEFFDQGYQC 415
QY	408 LKNGAVLLTVVRKGGDMSTMYVDYKTEDGSANAAGADYEFTGCTVYVLPKGETQKESVVG 467

Db	416	LENGCTVALTIRIRGCDLTNTYFVDFRTEDEGTANAGSDSYEFTEGTVFRKPGCTQKEIRVG	475
Qy	468	IIIDDDIEEEDHEFYRLSNVRIEEQPEEGMPALFNSLPLPRAYLASPCVATVTIILDD	527
	476	IIIDDDIEEEDENFLVHLTNSVKVSSSEASEDGILEANHVS---ALACLGSPSTATVTIIFDD	532
Qy	528	HAGITFECDTIHVSSEISGVMEVKVLRITSGARGIYVFRFVEGTAKKGGEDFEDTGYEL	587
	533	HAGITFEEDPYTHVSEISGIMEVKVLRITSGARGVIVPYKTIETGARCGGEDFEDTGCGL	592
Qy	588	EKKNDETV	595
	593	EFQNDETV	600

## RESULT 2

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Na+/Ca2+-exchanging protein precursor, cardiac - bovine
N:Alternate names: Na+/Ca2+ antiporter
C:Species: Bos primigenius taurus (cattle)
C>Date: 22-Nov-1993 #sequence=Levison 23-Mar-1995 #text.Change 18-Aug-2000
Accession: S27114; S18388
Aceto, J.F.; Condrescu, M.; Kroupis, C.; Nelson, H.; Nelson, N.; Nicoll, D.; Philipson
Arch. Biochem. Biophys. 298, 553-560, 1992
A>Title: Cloning and expression of the bovine cardiac sodium-calcium exchanger.
I:Reference number: S27114; PMID:93037494; PMID:1416984
A:Accession: S27114
A:Molecule type: mRNA
A:Residues: 1-970 <ACE>
A:Cross-references: GB:D06438, NID:g163033, PIDN:AAA30509.1; PID:g163034
R:Durkin, J.T.; Ahrens, D.C.; Pan, Y.C.E.; Reeves, J.P.
Arch. Biochem. Biophys. 290, 369-375, 1991
A>Title: Purification and amino-terminal sequence of the bovine cardiac sodium-calcium e
I:Reference number: S18388; PMID:9202750; PMID:1929404
A:Accession: S18388
A:Molecule type: Protein
A:Residues: 33-40,'X','42-44 <DUR>
A:Experimental source: heart
C:Superfamily: human Na+/Ca2+-exchanging protein
C:Keywords: cardiac muscle; heart; ion transport; membrane protein
F:1-32/Domin: signal sequence #status predicted <SIG>
F:33-970/Product: Na+/Ca2+ exchange protein, cardiac #status predicted <MNT>

Query Match      66.5%   Score 2147.5; DB 2; Length 970;
Best Local Similarity 69.4%; Pred. NO.2.4e-156;
Matches 422; Conservative 74; Mismatches 91; Indels 21; Gaps 8;

OY      1 MAMLRLOPLTSAFLHFGLVLELF--LNGLRKAGGSGDVSTQGNNECSGSSDCKEGV 58
        1 MLQPSLTPTSMGFHVIAIMVALLSFDHSVDHISAETEMEGNETGE---CTGYXXCKRGV 56

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QY 59 ILPLTWBENPBLGKRIANVIVYFVALYIMFGVSIILNDRFMASTEIVTSQREYTIKPN 118
Db 57 ILPLMEPDQPSFGDKIRATVYFVAMVYMFGLVSIILNDRFMASTEIVTSQREKTIKPN 116
QY 119 GETSTTIRWNEVYNSUTLALGSSAPEILSLIEVCGHGFAGDGLPSTIVGSAFNM 178
117 GETTKTVIRIMNEVYNSUTLALGSSAPEILSLYIEVCGHNFAGDGLPSTIVGSAFNM 176
QY 179 FIITIGCVYVRDEETRIKHLRYEFTIAMSITAYIMLYMILAVFSPGVQVWEGGLTL 238
177 FIILALCVYVRDEETRIKHLRYEFYTAAMSIFAYIMLYLISVSSPGVVEVEGLTLF 236
QY 239 FFFPVCVLLAAVAKRLLEYVYKMKKRYTDRKGLIITEGDHPKG---IEMDKMNSH 295
237 FFFPICVFAVNAVDRLLFFKYVYKRYRAGKQRMIIIEHEDBRSSKTEIEMDKVNSH 296
QY 296 ---FLDGNLVPLEGEWD---ESRREMIRILDKQNHPEKLDLDQVEMANYALASHOQ 348
297 VDSFLDALV-LEVDERDQDDEARREMARILKELQKHPEKEIEQILIANVULVSQOQ 355
QY 349 KSRAFYLIQATRMITGAGNIIKKHAEOAKKASSMEVNHDEPR-DTISKYFEDPCSTOC 407

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Db	356	KSMAFYRIQARLMTWAGANILKRHAADQARAKVASMHVEVNVEANDVSXIFFEQGIYQC	415
OY	408	LENGCAVLLTVYKRGDMKSTMYVDYITDGSANAGADYEFTBGTVLAKGFQKESVC	467
Db	416	LENGCTVALLTIIRKGGDLJTNVFPVDFRTEGTANAGSDYEFTBGTVVFKFGTEQKIRVG	475
OY	468	IIDDDIFEDEHFVYRLSNVRIIEEOPEBGMPIAFNSLPLPRVILASPCVATVITLDDO	527
Db	476	IIDDDIFEDEHFNLYHLSNVAVSLEASBEDGILENSHVS---TLACLAGSPSTATVITTFDDO	532
OY	528	HAGITFECDTIHVSESIGMEVKVRLTSGARGTIVFPRTVEGTAGAGGEDEFDYIGEL	587
Db	533	HAGITFEPEPTVHVSESIGIMEVKVRLTSGARGNVIVPYKTIEGTAGAGGEDEFDYIGEL	592
OY	588	EKKNDETV 595	
Db	593	EFQNDENV 600	

### RESULT 3

Na+/Ca2+-exchanging protein - human  
N:Alternate names: Na+/Ca2+ antiporter; Na+/Ca2+ exchanger  
C:Species: Homo sapiens (man)  
C:Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 17-Nov-2000  
C:Accession: S32815; A56767  
R:Komuro, I.; Wennlinger, K.E.; Philipson, K.D.; Izumo, S.  
Proc. Natl. Acad. Sci. U.S.A. 89, 4769-4773, 1992  
A:Title: Molecular cloning and characterization of the human cardiac Na(+/)Ca(2+) exchanger  
A:Reference number: S32815, MUID:92262521, PMID:1374913  
A:Accession: S32815  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-973 <ITU>  
A:Cross-references: EMBL:M91368; NID:g180672; PIDD:AAA35702.1; PUD:g180673  
R:Kotuji, P.; Hadley, R.W.; Kieval, R.S.; Lederer, W.J.; Schlize, D.H.  
Am. J. Physiol. 263, C1241-C1249, 1992  
A:Title: Expression of the Na-Ca exchanger in diverse tissues: a study using the clone  
A:Reference number: A56767; MUID:93118744; PMID:1476165  
A:Accession: A56767  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 47253,'K',255-627,'K',629-692,'K',694-973 <KOP>  
A:Note: sequence extracted from NCBI backbone (NCBIN:121126, NCBIPI:121127)  
C:Superfamily: human Na+/Ca2+-exchanging protein  
C:Keywords: cardiac muscle; heart; phosphoprotein; transmembrane protein

Query Match 66.5% Score 2146.5 DB 2 Length 973;  
Best Local Similarity 69.2% Pred. No. 2.9e-156;  
Matches 421; Conservative 76; Mismatches 90; Indels 21; Gaps 8;

[illegible]

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Db 300 VENFDGALV--LEVDERDODDEARREMARILKELKOKHPKEIQLEJLANYQVLSQQ 358
Oy 349 KSRATYRQATRTMTGAGNIIKKHAAEQAKKASSSEVHTDEPE--DFISKVFFDCCSTQC 407
Db 359 KSRATYRQATRTMTGAGNIIKKHAAEQAKKASSSEVHTDEPE--DFISKVFFDCCSTQC 418
Oy 408 LENCAGVLLTVRKGGDSKTMVYDKTTEGDSANAGADYEFTGTVVILKPGETQKEFSYG 467
Db 419 LENCSTVALTIIRRGDGLTNFYVDFRTEDGTANAGSDYEFTGTVVIRKPGDTQKEIRYG 478
Oy 468 IIDDIFEEDEHFVRLSNVRIEEOPEGMPPAIFNSLPLRAVLASPCVATVITLDD 527
Db 479 IIDDIFEEDEHFVRLSNVRIEEOPEGMPPAIFNSLPLRAVLASPCVATVITLDD 535
Oy 528 HAGITFEEDCDTHVSESGVMEVKLRTSGANGYIVPRRYEGTAKGGEFEDTTEL 587
Db 536 HAGITFEEDCDTHVSESGVMEVKLRTSGANGYIVPRRYEGTAKGGEFEDTTEL 595
Oy 588 EFKNDETV 595
Db 596 EFKNDETV 603

RESULT 4
148097
Na+/Ca2+-exchanging protein - guinea pig
C:Species: Cavia porcellus (guinea pig)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 18-Aug-2000
C:Accession: I48097
R:Tauruys, Y.; Bersohn, M.M.; Li, Z.; Nicoll, D.A.; Phillipson, K.D.
Biochim. Biophys. Acta 1196, 97-99, 1994
A:Title: Molecular cloning and functional expression of the guinea pig cardiac Na(+)-Ca2+
A:Reference number: I48097; MUID:95078257; PMID:7986817
A:Accession: I48097
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-970 <RES>
A:Cross-references: EMBL:U04955; NID:9927230; PIDN:AAA73904.1; PID:9507350
C:Superfamily: human Na+/Ca2+-exchanging protein

Query Match 66.4%; Score 2142.5; DB 2; Length 970;
Best Local Similarity 69.1%; Pred. No. 5.8e-156;
Matches 420; Conservative 76; Mismatches 91; Indels 21; Gaps 9;

Oy 1 MAMRLQGLTSAFLH--FGLVTFVL--FLNGLRARAGSGDVPSTGQNNSSGSSSCKCEV 58
Db 1 MRLSLSPYSLGFLHLLAMTLLISHVDHTAET---EMVEEGNETGECTGTSYCKRGV 56
Oy 59 ILPIWPNPNSLGDRIARIVYFVALIYMFGLVSIADRFMASIEVITSQREVTIKRPN 118
Db 57 ILPIWPNPNSLGDRIARIVYFVALIYMFGLVSIADRFMASIEVITSQREVTIKRPN 116
Oy 119 GETSTTTTRVWNETVSNLTLMALGSSAPRILSLIEVCGHGFIAGDLGPSTVGSAAFN 178
Db 117 GETTKTVIRWNETVSNLTLMALGSSAPRILSLIEVCGHGFIAGDLGPSTVGSAAFN 176
Oy 179 FLIIGICVYVPPDGETRRIKHLRVFFITPAWSIFAYIWMYLMILAFSPGVQVWEGGLTL 238
Db 177 FLIILACVYVPPDGETRRIKHLRVFFITPAWSIFAYIWMYLMILAFSPGVQVWEGGLTL 236
Oy 239 FFFPVCVLAVADRRLLEFYKMKHKYRTDKRGIIETEGDHPG---IENDGKMMNSH 295
Db 237 FFFPVCVLAVADRRLLEFYKMKHKYRTDKRGIIETEGDHPG---IENDGKMMNSH 296
Oy 296 ---FLDGLNVLPLEGKVD---ESRREMIRILKDKOKHPKEDLDQVLEMANVYALSHQ 348
Db 297 VENFDGALV--LEVDERDODDEARREMARILKELKOKHPKEIQLEJLANYQVLSQQ 355
Oy 349 KSRATYRQATRTMTGAGNIIKKHAAEQAKKASSSEVHTDEPE--DFISKVFFDCCSTQC 407
Db 356 KSRATYRQATRTMTGAGNIIKKHAAEQAKKASSSEVHTDEPE--DFISKVFFDCCSTQC 415
Oy 408 LENCAGVLLTVRKGGDSKTMVYDKTTEGDSANAGADYEFTGTVVILKPGETQKEFSYG 467
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Db 416 LENCSTVALTIIRRGDGLTNFYVDFRTEDGTANAGSDYEFTGTVVIRKPGDTQKEIRYG 475
Oy 468 IIDDIFEEDEHFVRLSNVRIEEOPEGMPPAIFNSLPLRAVLASPCVATVITLDD 527
Db 476 IIDDIFEEDEHFVRLSNVRIEEOPEGMPPAIFNSLPLRAVLASPCVATVITLDD 532
Oy 528 HAGITFEEDCDTHVSESGVMEVKLRTSGANGYIVPRRYEGTAKGGEFEDTTEL 587
Db 533 HAGITFEEDCDTHVSESGVMEVKLRTSGANGYIVPRRYEGTAKGGEFEDTTEL 592
Oy 588 EFKNDETV 595
Db 593 EFKNDETV 600

RESULT 5
A53789
Na+/Ca2+-exchanging protein precursor, splice form NACA7 - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 01-Dec-1995 #sequence_revision 01-Dec-1995 #text_change 18-Aug-2000
C:Accession: A53789; JX0288
R:Lee, S.L.; Yu, A.S.L.; Lytton, J.
J. Biol. Chem. 269, 14849-14852, 1994
A:Title: Tissue-specific expression of Na(+)-Ca(2+) exchanger isoforms.
A:Reference number: A53789; MUID:94253030; PMID:8195112
A:Accession: A53789
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-957 <LEP>
A:Cross-references: GB:U04933; NID:9451571; PIDN:AB39952.1; PID:9451572
R:Nakasaki, Y.; Yamoto, T.; Hanada, H.; Imagawa, T.; Shigekawa, M.
J. Biochem. 114, 528-534, 1993
A:Title: Cloning of the rat aortic smooth muscle Na+/Ca2+ exchanger and tissue-specific
A:Reference number: JX0288; MUID:94103175; PMID:8276763
A:Accession: JX0288
A:Molecule type: mRNA
A:Residues: 1-957 <NAK>
A:Experimental source: aortic smooth muscle
A:Superfamily: human Na+/Ca2+-exchanging protein
C:Keywords: ion transport; membrane protein
F:1-32/Domain: signal sequence #status predicted <SIG>
F:33-957/Product: Na+/Ca2+ exchanger #status predicted <MAT>

Query Match 66.2%; Score 2138; DB 2; Length 957;
Best Local Similarity 67.9%; Pred. No. 1.3e-155;
Matches 424; Conservative 73; Mismatches 87; Indels 40; Gaps 10;

Oy 4 LRLQGLTSAFLHFGVTFVFL-----NGLRARAGSGDVPSTGQNNSSGSSSCK 55
Db 2 LRLSLPYNVSKGFLVTLVALLFTVHDHTADTEAETGN-----ETTECTGTSYCK 53
Oy 56 EGVILPIWPNPNSLGDRIARIVYFVALIYMFGLVSIADRFMASIEVITSQREVTIK 115
Db 54 EGVILPIWPNPNSLGDRIARIVYFVALIYMFGLVSIADRFMASIEVITSQREVTIK 113
Oy 116 KPNGETSTTTTRVWNETVSNLTLMALGSSAPRILSLIEVCGHGFIAGDLGPSTVGSAA 175
Db 114 KPNGETSTTTTRVWNETVSNLTLMALGSSAPRILSLIEVCGHGFIAGDLGPSTVGSAA 173
Oy 176 FFMFLIIGICVYVPPDGETRRIKHLRVFFITPAWSIFAYIWMYLMILAFSPGVQVWEGGL 235
Db 174 FFMFLIIGICVYVPPDGETRRIKHLRVFFITPAWSIFAYIWMYLMILAFSPGVQVWEGGL 233
Oy 236 LTLFFPVCVLAVADRRLLEFYKMKHKYRTDKRGIIETEGDHPG---IENDGKMM 292
Db 234 LTLFFPVCVLAVADRRLLEFYKMKHKYRTDKRGIIETEGDHPG---IENDGKMM 293
Oy 293 NSH---FLDGLNVLPLEGKVD---ESRREMIRILKDKOKHPKEDLDQVLEMANVYALS 345
Db 294 NSH---FLDGLNVLPLEGKVD---ESRREMIRILKDKOKHPKEDLDQVLEMANVYALS 352
Oy 346 HQKSRATYRQATRTMTGAGNIIKKHAAEQAKKASSSEVHTDEPE--DFISKVFFDCCS 404
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|||||
Db 353 QOQKSRAFYRIQATRLMTGNTLKRHAADQARKAVSMHVNMDVVENDPVSVFEEQGT 412
Qy 405 YQCLNCGAVLLTVVRKGGMSKTMVYDKTEGDSANAGADYFETEGTVLAKGGEPOKEF 464
Db 413 YQCLNCGAVLALTIIRGGDLTNTVFVDFTEGDTANAGSDYFETEGTVLAKGGEPOKEF 472
Qy 465 SVGIIDDDIFEEDHFFVRLSNVRIEEOPEEGMPAIFNSLPUPR-AVLASPCVATVTI 523
Db 473 RVGIIDDDIFEEDHFFVRLSNVRIEEOPEEGMPAIFNSLPUPR-AVLASPCVATVTI 528
Qy 524 LDDHAGIFTEECDDTHVSESGVMEVKVLRITSGARCTVYVPRVTEGTAAGGGEDEFT 583
Db 529 FDDDHAGIFTEEPVYHVSESGVMEVKVLRITSGARCTVYVPRVTEGTAAGGGEDEFT 588
Qy 584 YGELEFRNDETV-----CDROE 600
Db 589 CGELEFRONDETVKTIITRIIDREE 612
```

## RESULT 6

53335

+/Ca2+-exchanging protein NCX1, splice form NCA6 - rabbit

C:Species: Oryctolagus cuniculus (domestic rabbit)

C:Date: 06-Oct-1994 #sequence\_revision 18-Nov-1994 #text\_change 18-Aug-2000

C:Accession: B53335

R:Kofuji, P.; Lederer, W.J.; Schulze, D.H.

J. Biol. Chem. 269, 5145-5149, 1994

A:Title: Mutually exclusive and cassette exons underlie alternatively spliced isoforms

A:Reference number: A53335; MID:94148976; PMID:8106495

A:Accession: B53335

A:Status: preliminary; not compared with conceptual translation

A:Molecule type: nucleic acid

A:Residues: 1-941 &lt;KOF&gt;

A:Experimental source: brain

A:Note: sequence extracted from NCBI backbone (NCBIP:144050)

C:Superfamily: human Na+/Ca2+-exchanging protein

Query Match 66.2%; Score 2136.5; DB 2; Length 941;

Best Local Similarity 69.5%; Pred. No. 1.6e-155;

Matches 417; Conservative 76; Mismatches 86; Indels 21; Gaps 9;

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Qy 8 PLTSAFLHGLVTFVLE-LNGLRAGSGDVPSTGQNNESGSSDCKEGLPLTWPE 66
Db 9 PFMGPFLLALVALFEFRVDHVASETMEGEENETGE---CTGSYYCKRGVILPIWEPQ 64
Qy 67 NPSLGKIAIVYFVALIYMLGVSIIADRPMASTEVITSOBERYTIKKPNGETSTTTI 126
Db 65 DPSFGDIATATYFVAMVYMLGVSIIADRPMSIEVITTSOKETITIK-NGETTKTV 123
Qy 127 RVNNETVSNLTLMALGSSAPEILLSTIEVCGHGFAGDLGPTIYVSAFNMFLIIGICY 186
Db 124 RINNETVSNLTLMALGSSAPEILLSTIEVCGHGFAGDLGPTIYVSAFNMFLIITACV 183
Qy 187 YVIPDETRKIKLRVFFITAAVSIFAYITWYILAVSPGVQVWEGILLTFEPVPCVL 246
Db 184 YVVPDETRKIKLRVFFITAAVSIFAYITWYILAVSPGVQVWEGILLTFEPVPCV 243
Qy 247 LAVVAACKRLFFYKMKKRYTDRKHGIIETEGDHPK---IEMDGMMNSH---FLDGN 300
Db 244 EAVVAACKRLFFYKMKKRYTDRKHGIIETEGDHPK---IEMDGMMNSH---FLDGN 303
Qy 301 LVPLEGEVD---ESRREMIRILDKOKHPEKDLQLEVMANYALSHQKSRAFYRI 356
Db 304 LV-LVNDERQDDEARREARILKELKOKHPEKDLQLEVMANYALSHQKSRAFYRI 362
Qy 357 QATRMATGAGNIIKHAQAQAKKASSMSEVHTDEP-DFISKVFDPSCSYQCLNCGAVL 415
Db 363 QATRMATGAGNIIKHAQAQAKKASSMSEVHTDEP-DFISKVFDPSCSYQCLNCGAVL 422
Qy 416 LTVVRKGGMSKTMVYDKTEGDSANAGADYFETEGTVLAKGGEPOKEFVGIIDDDIFE 475
Db 423 LTIIRGGDLTNTVFVDFTEGDTANAGSDYFETEGTVLAKGGEPOKEFVGIIDDDIFE 482
```

```
Qy 476 EDEHFFVRLSNVRIEEOPEEGMPAIFNSLPUPRAVLASPCVATVTIIDDHAGIETFE 535
Db 483 EDENFLVHLNSVAVSSETSDGILNANHIS---TLACLSGPTCATVYTFDDHAGIETFE 539
Qy 536 CDTHVSESGVMEVKVLRITSGARCTVYVPRVTEGTAAGGGEDEFTYGELEFRNDETV 585
Db 540 ESVTHVSESGVMEVKVLRITSGARCTVYVPRVTEGTAAGGGEDEFTYGELEFRNDETV 599
```

## RESULT 7

543730

Na+/Ca2+-exchanging protein - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 27-Jan-1995 #sequence\_revision 27-Jan-1995 #text\_change 18-Aug-2000

C:Accession: S43730

R:Purman, I.; Cook, O.; Kasir, J.; Rahamimoff, H.

FEBS Lett. 319, 105-109, 1993

A:Title: Cloning of two isoforms of the rat brain Na(+)-Ca(2+) exchanger gene and the

A:Reference number: S32435; MID:93202244; PMID:8454039

A:Accession: S43730

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-935 &lt;FUR&gt;

A:Dross-references: EMBL:X68812; NID:g288229; PIDN:CAA48707.1; PID:g288230

C:Superfamily: human Na+/Ca2+-exchanging protein

Query Match 66.2%; Score 2135.5; DB 2; Length 935;

Best Local Similarity 68.8%; Pred. No. 1.9e-155;

Matches 421; Conservative 72; Mismatches 86; Indels 33; Gaps 9;

```
Qy 4 LRLQPLTSAFLHGLVTFVLE-----NLGRAAGSGDVPSTGQNNESGSSDCK 55
Db 2 LRLSLPNSMGRFLVALFTVHDHTADTEAERGN-----ETTEGTSYVCK 53
Qy 56 EGYILTIWIPENSLGDKTARVYFVALIYMLGVSIIADRPMASTEVITSOBERYTIK 115
Db 54 KGVILPIWEPQDPSFGDKIARATVYFVAMVYMLGVSIIADRPMSIEVITTSOKETITIK 113
Qy 116 KPNGETSTTIRVNNETVSNLTLMALGSSAPEILLSTIEVCGHGFAGDLGPTIYVSA 175
Db 114 KPNGETSTTIRVNNETVSNLTLMALGSSAPEILLSTIEVCGHGFAGDLGPTIYVSA 173
Qy 176 FNMFIIGICVYVYVPGETRKIKLRVFFITAAVSIFAYITWYILAVSPGVQVWEG 235
Db 174 FNMFIIGICVYVYVPGETRKIKLRVFFITAAVSIFAYITWYILAVSPGVQVWEG 233
Qy 236 LTFEPVPCVLLAVADKRLFFYKMKKRYTDRKHGIIETEGDHPK---IEMDGMM 292
Db 234 LTFEPVPCVLLAVADKRLFFYKMKKRYTDRKHGIIETEGDHPK---IEMDGMM 293
Qy 293 NSH---FLOGNLVPLVSKGEVD---ESRREMIRILDKOKHPEKDLQLEVMANYAL 345
Db 294 NSHVDNFDLQALV-LEVDEFDQDDEARREARILKELKOKHPEKDLQLEVMANYAL 352
Qy 346 HQKSRAFYRIQATRLMTGAGNIIKHAQAQAKKASSMSEVHTDEP-DFISKVFDPSC 404
Db 353 QOQKSRAFYRIQATRLMTGAGNIIKHAQAQAKKASSMSEVHTDEP-DFISKVFDPSC 412
Qy 405 YQCLNCGAVLLTVVRKGGMSKTMVYDKTEGDSANAGADYFETEGTVLAKGGEPOKEF 464
Db 413 YQCLNCGAVLALTIIRGGDLTNTVFVDFTEGDTANAGSDYFETEGTVLAKGGEPOKEF 472
Qy 465 SVGIIDDDIFEEDHFFVRLSNVRIEEOPEEGMPAIFNSLPUPR-AVLASPCVATVTI 523
Db 473 RVGIIDDDIFEEDHFFVRLSNVRIEEOPEEGMPAIFNSLPUPR-AVLASPCVATVTI 528
Qy 524 LDDHAGIFTEECDDTHVSESGVMEVKVLRITSGARCTVYVPRVTEGTAAGGGEDEFT 583
Db 529 FDDDHAGIFTEEPVYHVSESGVMEVKVLRITSGARCTVYVPRVTEGTAAGGGEDEFT 588
Qy 584 YGELEFRNDETV 595
|||||
```

Db 589 CGELFEONDEIV 600

RESULT 8  
S32435  
Na+/Ca2+-exchanging protein RBE-2 - rat  
N:Alternate names: Na+/Ca2+ antiporter; sodium-calcium exchanger RBE-2  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 18-Aug-2000  
C:Accession: S32435  
R:Furman, I.; Cook, O.; Kasir, J.; Rahamimoff, H.  
FEBS Lett. 319, 105-109, 1993  
A:Title: Cloning of two isoforms of the rat brain Na(+) -Ca(2+) exchanger gene and their  
A:Reference numbers: S32435; MUID:93202244; PMID:8454033  
A:Accession: S32435  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-958 <PDB>  
C:Cross-references: EMBL:X68813; NID:g288231; PIDN:CAA48708.1; PID:g288232  
C:Superfamily: human Na+/Ca2+-exchanging protein

Query Match 66.2%; Score 2135.5; DB 2; Length 958;  
Best Local Similarity 68.8%; Pred. NO. 2e-15;  
Matches 421; Conservative 72; Mismatches 86; Indels 33; Gaps 9;

Db 4 LRLQPLTSFLHGLVTFYFL-----NGLRAEGSGDVPSTGQNNESCGSSDCK 55  
||| : : ||| | : ||| |  
Db 2 LRLSLPPNWSMGFRILVTLVALLFTYVDHTADTEAETGCGN-----ETTECTGSGYCK 53  
||| : : ||| | : ||| |  
Oy 56 EGVILPIVYRPMPSLGDKIAIYVYFVALIYMFGLSGIADRPMASIEVITSGREVTIK 115  
||| : : ||| | : ||| |  
Db 54 KGVILPIVPEQPSGDKIARATVYFVAWYVFLGSIADRPMSSIEVITSGKEITIK 113  
||| : : ||| | : ||| |  
Oy 116 KPNGETSTTTIYVNMETVSNLTLMALGSSAPILLSLIEVCGHGFAGDLGPESTYGSAA 175  
||| : : ||| | : ||| |  
Db 114 KPNGETTTTVAIMETVSNLTLMALGSSAPILLSLIEVCGHGFAGDLGPESTYGSAA 173  
||| : : ||| | : ||| |  
Oy 176 FNMFTIIGICVYVDPDGETRIKIKLRFEPITAAVSIFAYIWLIMILAVSPGVQVMEGL 235  
||| : : ||| | : ||| |  
Db 174 FNMFTIILCVYVDPDGETRIKIKLRFEPITAAVSIFAYITWLYIILSVSSPGVEVMEGL 233  
||| : : ||| | : ||| |  
Oy 236 LTFEFPVCVLLAWVADRKLFLYKYMHKYRFDKHNKGIIEFGDHPK---LEMDGKMA 292  
||| : : ||| | : ||| |  
Db 234 LTFEFPVCVFWAWADRRLFLYKYYKRYRAGKQGMIIIEHGDPRASKTEIEMDGKVA 293  
||| : : ||| | : ||| |  
Oy 293 NSH---FLDGNLVPLEGRKVD---ESREMRIRIKLDQKPERKLDLVEMANYALS 345  
||| : : ||| | : ||| |  
Db 294 NSHVNFLDGLALV-LEVDERDQDDEARREMARILKELQKHDKIEIOLIETLANQVUS 352  
||| : : ||| | : ||| |  
Oy 346 HQQSRATYRIQATIRMTGAGNIIKKHAAEQAKASSMSEVHTDEP-DETSKVFPPDS 404  
||| : : ||| | : ||| |  
Db 353 QOQKSRATYRIQATIRMTGAGNIIKKHAAEQAKASSMSEVHTDEP-DETSKVFPPDS 412  
||| : : ||| | : ||| |  
Oy 405 YQCLENCAGVLLTVYRKGGDMKTKYVDKTEDGSAACADVEFTGTIVYLKPGETOKER 464  
||| : : ||| | : ||| |  
Db 413 YQCLENCAGVALLTIRRGDLTNTVFDRTEBDGNAAGSDVEFTGTIVYFRGGEOKEL 472  
||| : : ||| | : ||| |  
Oy 465 SVGIIDDDIIFEDEHEFVLSNVRIEEOPREGMPAIFNSLPLR-AVLASCVATVIT 523  
||| : : ||| | : ||| |  
Db 473 RKGIIIDDDIIFEDEHEFVLSNVRISSEVSEDSG---ILDSNHSVAIACLGSPNTATIT 528  
||| : : ||| | : ||| |  
Oy 524 LDDDHAGIIFTEBCDITIHVESIGVMEVKVLTSGARGVIVPFRVETGAKGGEDFEDT 583  
||| : : ||| | : ||| |  
Db 529 FDDDHAGIIFTEBCDITIHVESIGVMEVKVLTSGARGVIVPFRVETGAKGGEDFEDT 588  
||| : : ||| | : ||| |  
Oy 584 YGELEFKNDEIV 595  
||| : : ||| | : ||| |  
Db 589 CGELFEONDEIV 600

RESULT 9  
S28833  
Na+/Ca2+-exchanging protein - rat

[illegible]





```
Db 598 WNKQLELVKKQSLRRPVKVMALGDLKSGDVAAES---TGERTDNEVK-----T 645
QY 303 PLECKEVEDSHREMIIRILKDLQKHPEKDDQVEMANYALSHQOK--SNAFYRIQATR 360
| 11: 11: 11: 11: 11: 11: 11: 11: 11: 11: 11: 11: 11: 11: 11:
Db 646 PGEENEGQSGE-----AQPEGEKEKENSEGDIQKERGENSEBDIAER 695
QY 361 MMTGAGNILLKHAQAQKASSMSEVHTDEPEDEISKVFPDPCSYQCLMCGAVLLTVR 420
| 11: 11: 11: 11: 11: 11: 11: 11: 11: 11: 11: 11: 11: 11: 11:
Db 696 KGDEG-----EGEIQAGEDEMKGDEGD-----LQAER 724
QY 421 KGDMSTMYVDYKTEGDSANAGADYEFTGTVLKPGETOKERSVGI-----IDD 471
| 11: 11: 11: 11: 11: 11: 11: 11: 11: 11: 11: 11: 11: 11: 11:
Db 725 KGDEGGEET--QAGEGEMK-GDDGETGQDLIADNQDAKEDKIDGEEGDSGESE 781
QY 472 DIFEDEHFFVRLSNVRIEEQPEE 496
| 11: 11: 11: 11: 11: 11: 11: 11: 11: 11: 11: 11: 11: 11: 11:
Db 782 DEEEEGEEEEGEEEGEEEGEE 806
```

## RESULT 15

S20969

Na+/Ca2+,K+-exchanging protein - bovine

Alternate names: Na+/Ca2+,K+ antiporter; Na/Ca,K-exchanger

C:Species: Bos primigenius taurus (cattle)

C:Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 05-Nov-1999

C:Accession: S20969

R:Releander, H.; Achilles, A.; Friedel, U.; Maul, G.; Lottspeich, F.; Cook, N.J.

EMBO J. 11, 1689-1695, 1992

A:Title: Primary structure and functional expression of the Na/Ca,K-exchanger from bovine

A:Reference number: S20969; MUID:92258377; PMID:1582405

A:Accession: S20969

A&gt;Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-1199 &lt;REI&gt;

A:Cross-references: GB:x66481; NID:g505578; PIDN:CAA47108.1; PID:g505579

Query Match 6.1%; Score 198.5; DB 2; Length 1199;

Best local similarity 21.7%; Pred. No. 1.1e-06;

Matches 132; Conservative 74; Mismatches 210; Indels 193; Gaps 27;

```
QY 77 VIVYFVALIMFVGVSIIADR-FMASIEVITSOBEREVTIKKPNGETSTTIRVNEVSN 135
| 11: 11: 11: 11: 11: 11: 11: 11: 11: 11: 11: 11: 11: 11: 11:
Db 449 VVLIHFGMMYVFVALAVCEYFPAVGITDK-----LQI-SEDVAG 490
QY 136 LTLALSSAPEILSLIEVCGHGFI-GDGPSTIVGSAFNMFTIGICVYIIPDET 194
| 11: 11: 11: 11: 11: 11: 11: 11: 11: 11: 11: 11: 11: 11: 11:
Db 491 ATFWAAGSAPELFTSLIGV---FISHSNVIGTIVGSAFNLIVYIGCALF-----S 541
QY 195 RKIKHLRVFFITAMSIFFAYIMLY---MLAVFSPGVVQVWEGLLTLEFFPVCL-LA 248
| 11: 11: 11: 11: 11: 11: 11: 11: 11: 11: 11: 11: 11: 11: 11:
| 11: 11: 11: 11: 11: 11: 11: 11: 11: 11: 11: 11: 11: 11: 11:
542 RELNL-----TWMPLEFROTFTYIFDLMLLEFFDLSTLAWMESVLLLAAYAFVFTMK 595
QY 249 WVADKRLLFYKYMKK-----YRTDKHRIITIEGDPKGIEMDKMNSHFLDG 299
| 11: 11: 11: 11: 11: 11: 11: 11: 11: 11: 11: 11: 11: 11: 11:
Db 596 WNOQLELVKKEQLKRPVAKVMALGDLKSGPDGTVVVDEQDNKKLKLSSMLTRG---S 651
QY 300 NLVPLECKEVEDSHRE-MIRILKDLQKHPEKDDQ--LVEMANYALSHQOKSRAFYRI 356
| 11: 11: 11: 11: 11: 11: 11: 11: 11: 11: 11: 11: 11: 11: 11:
Db 652 SSASLHNSITRSTIYQMLSHSLDPLGEARPSKDEEETLPEAK-----695
QY 357 QATRMMTAGNILLKHAQAQKASSMSEVHTDEPE-----DFISKVFDPDCSYQC 407
| 11: 11: 11: 11: 11: 11: 11: 11: 11: 11: 11: 11: 11: 11: 11:
Db 696 -----ATPQAKAESKPEEPKAKLEPTVTPAPAPADYKGDQEDPDGSGOV 739
QY 408 ---LENGC-----AVLLTVRKKGDMSTMYVDYKTEGDS---ANAGADYEFT 449
| 11: 11: 11: 11: 11: 11: 11: 11: 11: 11: 11: 11: 11: 11: 11:
Db 740 GAEAEANTGERTGAEAPAEENGERSGDALGSESEKAEENSEGDIPAERRGDDE-D 798
QY 450 EGTIVVLKPGETOKERSVGI-----DDDLFE-----EDEHFFVRLSNV 487
| 11: 11: 11: 11: 11: 11: 11: 11: 11: 11: 11: 11: 11: 11: 11:
Db 799 EGEIQAGEGEGYKDEGDEGETIQAGEGVEGEDEDE-----GEI 852
QY 488 RIEEEOPEEGMPAIFNSLPLPRAVLASPCVATVTIIDDHAGIFTECDTIHVESIGV 547
```

```
Db 853 QAGEAGEVEG-----DEDEGETIQAGEAGEVEGEDEDEGE 885
QY 548 MEVVLKLTSGARGYIVPFRVETAKG-----GDFEDTVELEFFKNDETVCDDQEA 601
| 11: 11: 11: 11: 11: 11: 11: 11: 11: 11: 11: 11: 11: 11: 11:
Db 886 IQ-----AGEGGEV-----KGESEIQAGEAGEVEGED-----GEVGGDEGETIQAGEG 930
QY 602 DYGRRGQOE 610
| 11: 11: 11: 11: 11: 11: 11: 11: 11: 11: 11: 11: 11: 11: 11:
Db 931 GEGETGEQE 939
```

Search completed: November 30, 2002, 12:32:11  
Job time: 24.3238 secs